Calibration of a Cybernetic Model Used for Modelling of Large Transient in an Activated Sludge Process

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Abstract Some publications have shown that the kinetic parameters of ASM models can be influenced by enzymatic regulation (Vanrolleghem et al., 1998; Haider et al., 2000; Lavallée et al., 2001). Therefore, an engineer aiming to make some modifications on a specific system is not able to predict the response of a real system after modifications have been made or cannot choose the right configuration or modifications on the basis of the current models. Thus, the objective of this paper is to present the calibration procedure of an activated sludge model which mimics the enzymatic induction of active biomass within the frame of ASM models. In the proposed model, process rates are modulated according to the environmental conditions and history of the cells. Data collected from short and long transient experiments were all fitted with a single set of parameters which was not possible with other models. The proposed model gives a more realistic picture of active biomass and of its specific activity under highly varying process conditions, but further research is required to support the model with experimental data

The ASM models (Henze et al., 2000) are based on Monod kinetics. Thus, the underlying hypothesis is that cells or active biomass possess only one metabolic state, or level of specific activity. According to the authors of ASM models, the parameters are intrinsically dependent on the operating conditions and the system configuration and have therefore to be evaluated for each of these. As cells regulate their metabolic state according to environmental conditions (Daigger and Grady, 1982; Grady et al., 1996), significant modifications of the operating conditions or of the process configuration will induce metabolic changes. These metabolic changes are not taken into account in the ASM models, and thus lead to discrepancies between simulations and real process behaviour. Also, nucleic acid probes are more and more often used in studies of wastewater treatment process and microbial ecology (Amann et al., 2000; Wilderer et al., 2002). So, quantification of active cells with probes will require models with further refinements in the description of active biomass, as variation of specific activity would been taken into account. The objective of this research is to propose modifications to the ASM by introducing enzymatic induction at the transcription level to model the variation of specific activity of cells. The aim of the proposed model is to mimic the varying specific growth rate of the active cells. With the proposed representation, parameter identification would become a procedure independent of sludge age, or independent of process configuration, which is not currently possible with the ASM.

Regulation of growth process is mainly associated to regulation of the protein synthesis system (PSS) (Zhang et al., 2002). So, the new feature of the model is a simplified representation of the PSS. A schematic of the PSS is given in Figure 1. According to this representation, the growth regulation of biomass depends on three main steps, i.e. the transport of substrate, the transcription and the translation mechanisms. A component with a short half life, messenger RNA (mRNA), is modeled by the variable *mR*. A component with a longer half life such as stable ribosomal RNA (rRNA) is modeled by the variable E_G. E_G will model the transcription and translation steps and the resulting increase in cells mass ($(1+E_G/X_H)*X_H$).

Rather than performing a simultaneous estimation of all parameters at once, the estimation problem is subdivided in different estimations of subsets of parameters. The subsets of parameters are constructed according to their relevant time constant. Evaluation of the rates can be performed using the oxygen consumption rate (rO_2), while the evaluation of the state variables is performed using COD measurements. The evaluation of active cells should be performed using DNA measurements. From the rO_2/DNA ratio it is possible to deduce the dynamics of variables such as *mR*, and E_G and to estimate the variation of the growth rate.

In figure 2 it is shown that it is possible to model transient behaviour of activated sludge during short-term batch experiments (Vanrolleghem et al., 1998). In this experiment, the sludge was first starved for 12 hours. Following the starvation period, 3 pulses of substrate were injected in the respirometer at time 0, 0.015 and 0.030 days. On the first and second pulse one can observe a gradual increase of the rO_2 or in other words of the growth rate until the added substrate is depleted, leading to the sudden drop of rO_2. As *mR* has a short time constant, the model was fitted on these data by changing the increase and decay rate of the variable *mR*. In the experiment depicted in figure 2, the available substrate is used for reconstruction of the *mR* pool raising the specific rO_2 after the starvation period. Using the same set of parameters used to fit the data of Vanroleghem et al. (1998), the model was also fitted on several transients in batch experiments extending over several hours (Chiu et al., 1973) (results not showed).

Experiments were also done in our laboratory to simulate a startup in a treatment system. A biomass was cultivated in a chemostat with an hydraulic residence time of 8 days; glucose was the sole source of carbon. To simulate a start-up, a transient was induced by applying a 5 times dilution of the biomass. The rO2 evaluation was done with a LSS respirometer (Spanjers et al., 1998). DNA was extracted according to Muttray et al. (2001). The DNA measurements were performed using bisbenzimide (Paul and Myers, 1982). Glucose and glycogen concentrations were evaluated using the anthrone method (Daniels et al., 1994). In figure 3, all data collected in the start-up experiment were fit simultaneously using the parameters values obtained in the fit to the data in the previous figure. Here, decay of cells and hydrolysis processes were introduced in the model. The response of the model is in good agreement with the COD and glycogen data. The increase of active cells COD (estimated using a ratio COD/DNA) is similar to the results but with a lag time of 4 days rather than 8 days.

A single set of parameter values can fit several experiments and can simultaneously model the variation of several components of the biomass. Thus, the chosen representation of the cells seems appropriate to model transient phenomena in the activated sludge process. The calibration procedure is subdivided in different estimations of subsets of parameters, and allows identification of the parameters according to their relevant time constant. Studies are under way and more experimental data will be shown in the full version of the paper.

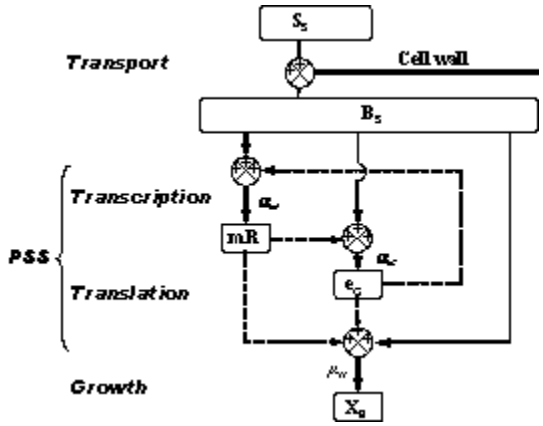

Figure 1 Schematic of the growth rate regulation mechanism

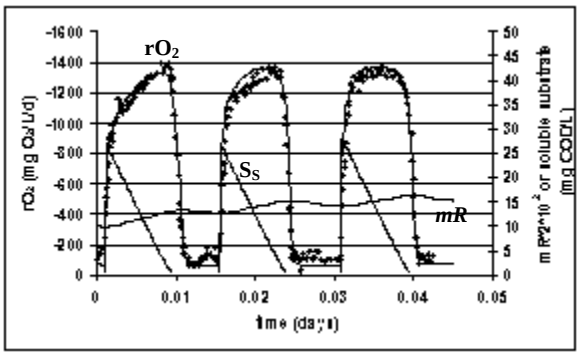

Figure 2 OUR start-up phenomena (data from Vanrolleghem et al., 1998).

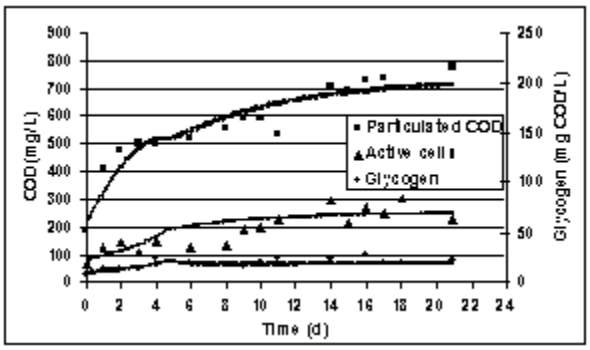

Figure 3 Fit of a start-up transient on a chemostat.

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